



## SEQUENCE LISTING

<110> Kline, Kimberly  
Sanders, Bob G.  
Yu, Weiping

<120> Mutant p53 Proteins And Uses Thereof

<130> D6454CIP

<140> US 10/696,255  
<141> 2003-10-29

<150> US 10/444,287  
<151> 2003-05-23

<160> 9

<210> 1  
<211> 1161  
<212> DNA  
<213> *Homo sapiens*

<220>  
<221> mat\_peptide  
<223> cDNA sequence of mutant p53 ( $\Delta$ 126-132)

<400> 1

atggaggagc	cgcagtcaga	tcctagcgtc	gagccccctc	tgagtcagga	50
aacattttca	gacctatgga	aactacttcc	tgaaaacaac	gttctgtccc	100
ccttgccgtc	ccaagcaatg	gatgatttga	tgctgtcccc	ggacgatatt	150
gaacaatggt	tactgaaga	cccaggcca	gatgaagctc	ccagaatgcc	200
agaggctgct	cccccggtg	cccctgcacc	agcagctcct	acaccggcgg	250
cccctgcacc	agccccctcc	tggccccctg	catctttctgt	cccttcccag	300
aaaacctacc	agggcagcta	cggtttccgt	ctgggcttct	tgcatctctg	350
gacagccaag	tctgtgactt	gcacgatgtt	ttgccaaactg	gccaagacct	400
gccctgtgca	gctgtgggtt	gattccacac	ccccgcccgg	caccgcgctc	450
cgcgccatgg	ccatctacaa	gcagtcacag	cacatgacgg	aggttgtgag	500
gcgctgcccc	caccatgagc	gctgctcaga	tagcgatggt	ctggccccctc	550
ctcagcatct	tatccgagtg	gaaggaaatt	tgctgttgga	gtatttggat	600
gacagaaaca	cttttcgaca	tagtgtgtgtg	gtgccctatg	agccgcctga	650
ggttggtctt	gactgtacca	ccatccacta	caactacatg	tgtaacagtt	700
cctgcattgg	cggcatgaac	cggaggccca	tcctcaccat	catcacactg	750
gaagactcca	gtggtaattt	actgggacgg	aacagctttg	agggtgatgt	800
ttgtgcctgt	cctgggagag	accggcgcac	agaggaagag	aatctccgca	850
agaaagggga	gcctcaccac	gagctgcccc	caggagacac	taagcgagca	900
ctgcccacaa	acaccagctc	ctctccccag	ccaaagaaga	aaccactgga	950
tggagaatat	ttcacccttc	agatccgtgg	gcgtgagcgc	ttcgagatgt	1000
tccgagagct	gaatgaggcc	ttggaactca	aggatgccca	ggctgggaag	1050
gagccagggg	ggagcagggc	tactccagc	cacctgaagt	ccaaaaaggg	1100
tcagtctacc	tcccgccata	aaaaactcat	gttcaagaca	gaagggcctg	1150
actcagactg	a				1161

<210> 2  
 <211> 386  
 <212> PRT  
 <213> *Homo sapiens*  
  
 <220>  
 <221> PEPTIDE  
 <223> mutant p53 ( $\Delta$ 126-132)

<400> 2  
 Met Glu Glu Pro Gln Ser Asp Pro Ser Val Glu Pro Pro Leu Ser  
                   5                  10                  15  
 Gln Glu Thr Phe Ser Asp Leu Trp Lys Leu Leu Pro Glu Asn Asn  
                   20                  25                  30  
 Val Leu Ser Pro Leu Pro Ser Gln Ala Met Asp Asp Leu Met Leu  
                   35                  40                  45  
 Ser Pro Asp Asp Ile Glu Gln Trp Phe Thr Glu Asp Pro Gly Pro  
                   50                  55                  60  
 Asp Glu Ala Pro Arg Met Pro Glu Ala Ala Pro Pro Val Ala Pro  
                   65                  70                  75  
 Ala Pro Ala Ala Pro Thr Pro Ala Ala Pro Ala Pro Ala Pro Ser  
                   80                  85                  90  
 Trp Pro Leu Ser Ser Ser Val Pro Ser Gln Lys Thr Tyr Gln Gly  
                   95                  100                 105  
 Ser Tyr Gly Phe Arg Leu Gly Phe Leu His Ser Gly Thr Ala Lys  
                  110                 115                 120  
 Ser Val Thr Cys Thr Met Phe Cys Gln Leu Ala Lys Thr Cys Pro  
                  125                 130                 135  
 Val Gln Leu Trp Val Asp Ser Thr Pro Pro Pro Gly Thr Arg Val  
                  140                 145                 150  
 Arg Ala Met Ala Ile Tyr Lys Gln Ser Gln His Met Thr Glu Val  
                  155                 160                 165  
 Val Arg Arg Cys Pro His His Glu Arg Cys Ser Asp Ser Asp Gly  
                  170                 175                 180  
 Leu Ala Pro Pro Gln His Leu Ile Arg Val Glu Gly Asn Leu Arg  
                  185                 190                 195  
 Val Glu Tyr Leu Asp Asp Arg Asn Thr Phe Arg His Ser Val Val  
                  200                 205                 210  
 Val Pro Tyr Glu Pro Pro Glu Val Gly Ser Asp Cys Thr Thr Ile  
                  215                 220                 225  
 His Tyr Asn Tyr Met Cys Asn Ser Ser Cys Met Gly Gly Met Asn  
                  230                 235                 240  
 Arg Arg Pro Ile Leu Thr Ile Ile Thr Leu Glu Asp Ser Ser Gly  
                  245                 250                 255  
 Asn Leu Leu Gly Arg Asn Ser Phe Glu Val His Val Cys Ala Cys  
                  260                 265                 270  
 Pro Gly Arg Asp Arg Arg Thr Glu Glu Glu Asn Leu Arg Lys Lys  
                  275                 280                 285  
 Gly Glu Pro His His Glu Leu Pro Pro Gly Ser Thr Lys Arg Ala  
                  290                 295                 300

Leu	Pro	Asn	Asn	Thr	Ser	Ser	Ser	Pro	Gln	Pro	Lys	Lys	Lys	Pro
				305					310					315
Leu	Asp	Gly	Glu	Tyr	Phe	Thr	Leu	Gln	Ile	Arg	Gly	Arg	Glu	Arg
				320					325					330
Phe	Glu	Met	Phe	Arg	Glu	Leu	Asn	Glu	Ala	Leu	Glu	Leu	Lys	Asp
				335					340					345
Ala	Gln	Ala	Gly	Lys	Glu	Pro	Gly	Gly	Ser	Arg	Ala	His	Ser	Ser
				350					355					360
His	Leu	Lys	Ser	Lys	Lys	Gly	Gln	Ser	Thr	Ser	Arg	His	Lys	Lys
				365					370					375
Leu	Met	Phe	Lys	Thr	Glu	Gly	Pro	Asp	Ser	Asp				
				380					385					

<210> 3  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> primer\_bind  
 <223> sense primer for p53

<400> 3  
 atggaggagc cgagtcaga t 21

<210> 4  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> primer\_bind  
 <223> anti-sense primer for p53

<400> 4  
 tcagtctgag tcaggccctt c 21

<210> 5  
 <211> 60  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> primer\_bind  
 <223> sense primer for p53, encoding an EcoRI restriction enzyme cutting site, starting codon, HA residue, and p53 sequence from 4-21 nucleotide bases

<400> 5  
 cgcgattca tgtatgatgt tcctgattat gctagcctcg aggagccgca 50  
 gtcagatcct 60

```

<210>      6
<211>      30
<212>      DNA
<213>      Artificial Sequence

<220>
<221>      primer_bind
<223>      anti-sense primer for p53, containing a BamHI
restriction enzyme cutting site and stop codon

<400>      6
cgcggtatcct cagtctgagt caggcccttc      30

<210>      7
<211>      392
<212>      PRT
<213>      Homo sapiens

<220>
<221>      PEPTIDE
<223>      wild-type p53

<400>      7
Met Glu Glu Pro Gln Ser Asp Pro Ser Val Glu Pro Pro Leu Ser
      5      10      15
Gln Glu Thr Phe Ser Asp Leu Trp Lys Leu Leu Pro Glu Asn Asn
      20      25      30
Val Leu Ser Pro Leu Pro Ser Gln Ala Met Asp Asp Leu Met Leu
      35      40      45
Ser Pro Asp Asp Ile Glu Gln Trp Phe Thr Glu Asp Pro Gly Pro
      50      55      60
Asp Glu Ala Pro Arg Met Pro Glu Ala Ala Pro Pro Val Ala Pro
      65      70      75
Ala Pro Ala Ala Pro Thr Pro Ala Ala Pro Ala Pro Ala Pro Ser
      80      85      90
Trp Pro Leu Ser Ser Ser Val Pro Ser Gln Lys Thr Tyr Gln Gly
      95     100     105
Ser Tyr Gly Phe Arg Leu Gly Phe Leu Ser Gly Thr Ala Lys Ser
      110     115     120
Val Thr Cys Thr Tyr Ser Pro Ala Leu Asn Lys Met Phe Cys Gln
      125     130     135
Leu Ala Lys Thr Cys Pro Val Gln Leu Trp Val Asp Ser Thr Pro
      140     145     150
Pro Pro Gly Thr Arg Val Arg Ala Met Ala Ile Tyr Lys Gln Ser
      155     160     165
Gln His Met Thr Glu Val Val Arg Arg Cys Pro His His Glu Arg
      170     175     180
Cys Ser Asp Ser Asp Gly Leu Ala Pro Pro Gln His Leu Ile Arg
      185     190     195
Val Glu Gly Asn Leu Arg Val Glu Tyr Leu Asp Asp Arg Asn Thr
      200     205     210

```

Phe	Arg	His	Ser	Val	Val	Val	Pro	Tyr	Glu	Pro	Pro	Glu	Val	Gly
				215					220					225
Ser	Asp	Cys	Thr	Thr	Ile	His	Tyr	Asn	Tyr	Met	Cys	Asn	Ser	Ser
				230					235					240
Cys	Met	Gly	Gly	Met	Asn	Arg	Arg	Pro	Ile	Leu	Thr	Ile	Ile	Thr
				245					250					255
Leu	Glu	Asp	Ser	Ser	Gly	Asn	Leu	Leu	Gly	Arg	Asn	Ser	Phe	Glu
				260					265					270
Val	Arg	Val	Cys	Ala	Cys	Pro	Gly	Arg	Asp	Arg	Arg	Thr	Glu	Glu
				275					280					285
Glu	Asn	Leu	Arg	Lys	Lys	Gly	Glu	Pro	His	His	Glu	Leu	Pro	Pro
				290					295					300
Gly	Ser	Thr	Lys	Arg	Ala	Leu	Pro	Asn	Asn	Thr	Ser	Ser	Ser	Pro
				305					310					315
Gln	Pro	Lys	Lys	Lys	Pro	Leu	Asp	Gly	Glu	Tyr	Phe	Thr	Leu	Gln
				320					325					330
Ile	Arg	Gly	Arg	Glu	Arg	Phe	Glu	Met	Phe	Arg	Glu	Leu	Asn	Glu
				335					340					345
Ala	Leu	Glu	Leu	Lys	Asp	Ala	Gln	Ala	Gly	Lys	Glu	Pro	Gly	Gly
				350					355					360
Ser	Arg	Ala	His	Ser	Ser	His	Leu	Lys	Ser	Lys	Lys	Gly	Gln	Ser
				365					370					375
Thr	Ser	Arg	His	Lys	Lys	Leu	Met	Phe	Lys	Thr	Glu	Gly	Pro	Asp
				380					385					390
Ser	Asp													

<210> 8  
 <211> 358  
 <212> PRT  
 <213> *Homo sapiens*

<220>  
 <221> PEPTIDE  
 <223> p53 double mutant ( $\Delta$ 126-132+ $\Delta$ 367-393)

Met	Glu	Glu	Pro	Gln	Ser	Asp	Pro	Ser	Val	Glu	Pro	Pro	Leu	Ser
				5					10					15
Gln	Glu	Thr	Phe	Ser	Asp	Leu	Trp	Lys	Leu	Leu	Pro	Glu	Asn	Asn
				20					25					30
Val	Leu	Ser	Pro	Leu	Pro	Ser	Gln	Ala	Met	Asp	Asp	Leu	Met	Leu
				35					40					45
Ser	Pro	Asp	Asp	Ile	Glu	Gln	Trp	Phe	Thr	Glu	Asp	Pro	Gly	Pro
				50					55					60
Asp	Glu	Ala	Pro	Arg	Met	Pro	Glu	Ala	Ala	Pro	Pro	Val	Ala	Pro
				65					70					75
Ala	Pro	Ala	Ala	Pro	Thr	Pro	Ala	Ala	Pro	Ala	Pro	Ala	Pro	Ser
				80					85					90
Trp	Pro	Leu	Ser	Ser	Ser	Val	Pro	Ser	Gln	Lys	Thr	Tyr	Gln	Gly
				95					100					105
Ser	Tyr	Gly	Phe	Arg	Leu	Gly	Phe	Leu	Ser	Gly	Thr	Ala	Lys	Ser
				110					115					120

Val	Thr	Cys	Thr	Met	Phe	Cys	Gln	Leu	Ala	Lys	Thr	Cys	Pro	Val	
				125					130					135	
Gln	Leu	Trp	Val	Asp	Ser	Thr	Pro	Pro	Pro	Gly	Thr	Arg	Val	Arg	
				140					145					150	
Ala	Met	Ala	Ile	Tyr	Lys	Gln	Ser	Gln	His	Met	Thr	Glu	Val	Val	
				155					160					165	
Arg	Arg	Cys	Pro	His	His	Glu	Arg	Cys	Ser	Asp	Ser	Asp	Gly	Leu	
				170					175					180	
Ala	Pro	Pro	Gln	His	Leu	Ile	Arg	Val	Glu	Gly	Asn	Leu	Arg	Val	
				185					190					195	
Glu	Tyr	Leu	Asp	Asp	Arg	Asn	Thr	Phe	Arg	His	Ser	Val	Val	Val	
				200					205					210	
Pro	Tyr	Glu	Pro	Pro	Glu	Val	Gly	Ser	Asp	Cys	Thr	Thr	Ile	His	
				215					220					225	
Tyr	Asn	Tyr	Met	Cys	Asn	Ser	Ser	Cys	Met	Gly	Gly	Met	Asn	Arg	
				230					235					240	
Arg	Pro	Ile	Leu	Thr	Ile	Ile	Thr	Leu	Glu	Asp	Ser	Ser	Gly	Asn	
				245					250					255	
Leu	Leu	Gly	Arg	Asn	Ser	Phe	Glu	Val	Arg	Val	Cys	Ala	Cys	Pro	
				260					265					270	
Gly	Arg	Asp	Arg	Arg	Thr	Glu	Glu	Glu	Asn	Leu	Arg	Lys	Lys	Gly	
				275					280					285	
Glu	Pro	His	His	Glu	Leu	Pro	Pro	Gly	Ser	Thr	Lys	Arg	Ala	Leu	
				290					295					300	
Pro	Asn	Asn	Thr	Ser	Ser	Ser	Pro	Gln	Pro	Lys	Lys	Lys	Pro	Leu	
				305					310					315	
Asp	Gly	Glu	Tyr	Phe	Thr	Leu	Gln	Ile	Arg	Gly	Arg	Glu	Arg	Phe	
				320					325					330	
Glu	Met	Phe	Arg	Glu	Leu	Asn	Glu	Ala	Leu	Glu	Leu	Lys	Asp	Ala	
				335					340					345	
Gln	Ala	Gly	Lys	Glu	Pro	Gly	Gly	Ser	Arg	Ala	His	Ser			
				350					355						

<210> 9  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> primer\_bind  
 <223> anti-sense primer for TM p53 and p53 double mutant

<400> 9  
 gcgtctagat caggagttag cctgctccc 30